

Angelo Toto

List of Publications by Year in descending order

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623734

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docs citations

46
times ranked

865
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#	ARTICLE	IF	CITATIONS
1	Unveiling induced folding of intrinsically disordered proteins â€“ Protein engineering, frustration and emerging themes. <i>Current Opinion in Structural Biology</i> , 2022, 72, 153-160.	5.7	15
2	On the Effects of Disordered Tails, Supertertiary Structure and Quinary Interactions on the Folding and Function of Protein Domains. <i>Biomolecules</i> , 2022, 12, 209.	4.0	5
3	Anticancer Activity of (S)-5-Chloro-3-((3,5-dimethylphenyl)sulfonyl)-N-(1-oxo-1-((pyridin-4-ylmethyl)amino)propan-2-yl)-1H-indole-2-carboxamide (RS4690), a New Dishevelled 1 Inhibitor. <i>Cancers</i> , 2022, 14, 1358.		4
4	Characterization of early and late transition states of the folding pathway of a <sc>SH2</sc> domain. <i>Protein Science</i> , 2022, 31, .	7.6	4
5	Structural determinants driving the binding process between PDZ domain of wild type human PALS1 protein and SLiM sequences of SARS-CoV E proteins. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 1838-1847.	4.1	11
6	Double Mutant Cycles as a Tool to Address Folding, Binding, and Allostery. <i>International Journal of Molecular Sciences</i> , 2021, 22, 828.	4.1	17
7	Folding and Misfolding of a PDZ Tandem Repeat. <i>Journal of Molecular Biology</i> , 2021, 433, 166862.	4.2	8
8	Probing the Effects of Local Frustration in the Folding of a Multidomain Protein. <i>Journal of Molecular Biology</i> , 2021, 433, 167087.	4.2	6
9	Determining folding and binding properties of the C-terminal SH2 domain of SHP2. <i>Protein Science</i> , 2021, 30, 2385-2395.	7.6	6
10	Targeting PDZ domains as potential treatment for viral infections, neurodegeneration and cancer. <i>Biology Direct</i> , 2021, 16, 15.	4.6	12
11	Experimental Characterization of the Interaction between the N-Terminal SH3 Domain of Crkl and C3G. <i>International Journal of Molecular Sciences</i> , 2021, 22, 13174.	4.1	1
12	The Effect of Proline cis-trans Isomerization on the Folding of the C-Terminal SH2 Domain from p85. <i>International Journal of Molecular Sciences</i> , 2020, 21, 125.	4.1	3
13	Hidden kinetic traps in multidomain folding highlight the presence of a misfolded but functionally competent intermediate. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 19963-19969.	7.1	16
14	Comparing the binding properties of peptides mimicking the Envelope protein of <sc>SARSâ€CoV</sc> and <sc>SARSâ€CoV</sc>â€2 to the <sc>PDZ</sc> domain of the tight junctionâ€associated <sc>PALS1</sc> protein. <i>Protein Science</i> , 2020, 29, 2038-2042.	7.6	48
15	Targeting the Interaction between the SH3 Domain of Grb2 and Gab2. <i>Cells</i> , 2020, 9, 2435.	4.1	7
16	Understanding the Binding Induced Folding of Intrinsically Disordered Proteins by Protein Engineering: Caveats and Pitfalls. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3484.	4.1	11
17	Understanding the Mechanism of Recognition of Gab2 by the N-SH2 Domain of SHP2. <i>Life</i> , 2020, 10, 85.	2.4	6
18	Unveiling the Molecular Basis of the Noonan Syndrome-Causing Mutation T42A of SHP2. <i>International Journal of Molecular Sciences</i> , 2020, 21, 461.	4.1	23

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19	Templated folding of intrinsically disordered proteins. <i>Journal of Biological Chemistry</i> , 2020, 295, 6586-6593.	3.4	44
20	Demonstration of Binding Induced Structural Plasticity in a SH2 Domain. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 89.	3.5	5
21	Understanding Binding-Induced Folding by Temperature Jump. <i>Methods in Molecular Biology</i> , 2020, 2141, 651-661.	0.9	0
22	Structural characterization of an onâ€­pathway intermediate and transition state in the folding of the Nâ€­terminal SH2 domain from SHP2. <i>FEBS Journal</i> , 2019, 286, 4769-4777.	4.7	7
23	Binding induced folding: Lessons from the kinetics of interaction between NTAIL and XD. <i>Archives of Biochemistry and Biophysics</i> , 2019, 671, 255-261.	3.0	9
24	Investigating the Molecular Basis of the Aggregation Propensity of the Pathological D76N Mutant of Beta-2 Microglobulin: Role of the Denatured State. <i>International Journal of Molecular Sciences</i> , 2019, 20, 396.	4.1	5
25	Mapping the allosteric network within a SH3 domain. <i>Scientific Reports</i> , 2019, 9, 8279.	3.3	18
26	Characterization of human frataxin missense variants in cancer tissues. <i>Human Mutation</i> , 2019, 40, 1400-1413.	2.5	16
27	The kinetics of folding of the NSH2 domain from p85. <i>Scientific Reports</i> , 2019, 9, 4058.	3.3	9
28	Folding mechanisms steer the amyloid fibril formation propensity of highly homologous proteins. <i>Chemical Science</i> , 2018, 9, 3290-3298.	7.4	18
29	Stability of an aggregation-prone partially folded state of human profilin-1 correlates with aggregation propensity. <i>Journal of Biological Chemistry</i> , 2018, 293, 10303-10313.	3.4	10
30	Mechanism of Folding and Binding of the N-Terminal SH2 Domain from SHP2. <i>Journal of Physical Chemistry B</i> , 2018, 122, 11108-11114.	2.6	19
31	Folding Mechanism of the SH3 Domain from Grb2. <i>Journal of Physical Chemistry B</i> , 2018, 122, 11166-11173.	2.6	9
32	Understanding the role of phosphorylation in the binding mechanism of a PDZ domain. <i>Protein Engineering, Design and Selection</i> , 2017, 30, 1-5.	2.1	11
33	The Folding Pathway of the KIX Domain. <i>ACS Chemical Biology</i> , 2017, 12, 1683-1690.	3.4	6
34	Regulation of the Human Phosphatase PTPN4 by the inter-domain linker connecting the PDZ and the phosphatase domains. <i>Scientific Reports</i> , 2017, 7, 7875.	3.3	12
35	Analyzing the Folding and Binding Steps of an Intrinsically Disordered Protein by Protein Engineering. <i>Biochemistry</i> , 2017, 56, 3780-3786.	2.5	28
36	Understanding the mechanism of binding between Gab2 and the C terminal SH3 domain from Grb2. <i>Oncotarget</i> , 2017, 8, 82344-82351.	1.8	10

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37	Ligand binding to the PDZ domains of postsynaptic density protein 95. <i>Protein Engineering, Design and Selection</i> , 2016, 29, 169-175.	2.1	13
38	Activation Barrier-Limited Folding and Conformational Sampling of a Dynamic Protein Domain. <i>Biochemistry</i> , 2016, 55, 5289-5295.	2.5	14
39	Molecular Recognition by Templated Folding of an Intrinsically Disordered Protein. <i>Scientific Reports</i> , 2016, 6, 21994.	3.3	87
40	Mutational Analysis of the Binding-Induced Folding Reaction of the Mixed-Lineage Leukemia Protein to the KIX Domain. <i>Biochemistry</i> , 2016, 55, 3957-3962.	2.5	19
41	Understanding the effect of alternative splicing in the folding and function of the second PDZ from Protein Tyrosine Phosphatase-BL. <i>Scientific Reports</i> , 2015, 5, 9299.	3.3	4
42	The mechanism of binding of the second PDZ domain from the Protein Tyrosine Phosphatase-BL to the Adenomatous Polyposis Coli tumor suppressor. <i>Protein Engineering, Design and Selection</i> , 2014, 27, 249-253.	2.1	3
43	The mechanism of binding of the KIX domain to the mixed lineage leukemia protein and its allosteric role in the recognition of c-Myb. <i>Protein Science</i> , 2014, 23, 962-969.	7.6	38
44	The kinetics of folding of frataxin. <i>Physical Chemistry Chemical Physics</i> , 2014, 16, 6391.	2.8	17
45	Understanding the frustration arising from the competition between function, misfolding, and aggregation in a globular protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 14141-14146.	7.1	43
46	Structure of the transition state for the binding of c-Myb and KIX highlights an unexpected order for a disordered system. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 14942-14947.	7.1	99